

Serial Number: 09/522,7270

CRF Processing Date: 7/22/2002  
Edited by: AE  
Verified by: AE (STIC staff)**ENTERED**

P#31

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Seq 54 - corrected amino acid numbering

**RECEIVED**

JUL 26 2002

TECH CENTER 1600/2900

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/522,727D

DATE: 07/22/2002

TIME: 14:04:28

Input Set : A:\EP.txt

Output Set: N:\CRF3\07222002\I522727D.raw

**Does Not Comply**  
**Corrected Diskette Needed**

4 <110> APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.  
 5 MARASCO, Wayne  
 6 MHASHILKAR, Abner  
 8 <120> TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE REACTIONS  
 10 <130> FILE REFERENCE: 47577 C  
 12 <140> CURRENT APPLICATION NUMBER: 09/522,727D  
 13 <141> CURRENT FILING DATE: 2000-03-10  
 15 <150> PRIOR APPLICATION NUMBER: PCT/US98/19563  
 16 <151> PRIOR FILING DATE: 1998-09-18  
 18 <150> PRIOR APPLICATION NUMBER: 60/059,339  
 19 <151> PRIOR FILING DATE: 1997-09-19  
 21 <160> NUMBER OF SEQ ID NOS: 56  
 23 <170> SOFTWARE: PatentIn version 3.1

## ERRORED SEQUENCES

698 <210> SEQ ID NO: 54  
 699 <211> LENGTH: 277  
 700 <212> TYPE: PRT  
 701 <213> ORGANISM: human  
 703 <400> SEQUENCE: 54  
 704 Met Glu His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 705 1 5 10 15  
 706 Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Thr Arg  
 707 20 25 30  
 708 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 709 35 40 45  
 710 Thr Ser His Trp Met Gln Trp Val Arg Gln Arg Pro Gly Gln Gly Leu  
 711 50 55 60  
 712 Glu Trp Ile Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr  
 713 65 70 75 80  
 714 Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr  
 715 85 90 95  
 716 Thr Ala Tyr Leu His Leu Ser Ser Leu Ser Ser Glu Asp Ser Ala Val  
 E--> 717 100 105 ~~110~~ 110  
 718 Tyr Tyr Cys Ala Arg Asp Glu Ile Thr Thr Val Val Pro Arg Gly Phe  
 E--> 719 115 120 125  
 720 Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly  
 E--> 721 130 135 140  
 722 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu  
 E--> 723 145 150 155 160  
 724 Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Thr Ile Thr

*← misaligned amino  
 acid  
 nos.*

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DATE: 07/22/2002

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TIME: 14:04:28

Input Set : A:\EP.txt

Output Set: N:\CRF3\07222002\I522727D.raw

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E--> 725          165          170          175
      726 Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser Trp Tyr
E--> 727          180          185          190
      728 Gln Gln Lys Pro Gly Asn Ile Pro Gln Leu Leu Ile Tyr Lys Ala Ser
E--> 729          195          200          205
      730 Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly
E--> 731          210          215          220
      732 Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Gly
E--> 733 225          230          235          240
      734 Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Leu Thr Phe Gly Gly
E--> 735          245          250          255
      736 Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser
E--> 737          260          265          270
      738 Glu Lys Asp Glu Leu
      750 <210> SEQ ID NO: 56
      751 <211> LENGTH: 8
      752 <212> TYPE: PRT
      753 <213> ORGANISM: human
      755 <400> SEQUENCE: 56
      756 Ser Ile Ile Asn Phe Glu Lys Leu
      757 1          5
E--> 762 (Footnote continued from previous page)
E--> 763 (Footnote continued on next page)

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*delete*

## VERIFICATION SUMMARY

DATE: 07/22/2002

PATENT APPLICATION: US/09/522,727D

TIME: 14:04:30

Input Set : A:\EP.txt

Output Set: N:\CRF3\07222002\I522727D.raw

L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0  
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:16  
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:480  
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:528  
L:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:160  
L:717 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54  
M:332 Repeated in SeqNo=54  
L:762 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:762 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:5  
L:763 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:56  
L:763 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:763 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:5  
L:763 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:18 SEQ:56